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Evaluation of the hygienic performances of the processes for cleaning, dressing and cooling pig carcasses at eight packing plants

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Abstract

The hygienic performances of the processes for the production of cooled carcasses at eight pork packing plants were assessed from small sets of microbiological data. At each plant, a single sample was obtained from a randomly selected site on each of 25 randomly selected carcasses at each of three stages of processing, which were after polishing, after washing at the end of the dressing process, and after cooling. The aerobic bacteria, coliforms and *Escherichia coli* recovered from each sample were enumerated. When bacteria of one type were recovered from ≥ 20 of 25 samples, the log mean number of those bacteria on the population of carcasses undergoing processing was estimated on the assumption that the set of counts was normally distributed. The log of the total number recovered from 25 samples was calculated for each set of counts. The log mean numbers of total aerobic bacteria recovered from the polished carcasses at different plants ranged from about 1.9 to 3.8 log cfu cm^{-2}. At six of the plants, the log mean numbers of total aerobes on the cooled carcasses did not differ substantially from the log mean numbers on the polished carcasses, but the log mean numbers on the cooled carcasses were substantially higher at one plant and substantially lower at another than on the polished carcasses. Coliforms and *E. coli* were recovered from too few samples in most sets from cooled carcasses for estimation of their log mean numbers. However, the log total numbers of coliforms and *E. coli* recovered indicated that substantial numbers of those organisms were added to carcasses during the dressing processes at four of the plants, and that the numbers on the carcasses were substantially reduced by the processes for cooling without spraying at two of the plants. At seven of the plants, the total numbers of coliforms and *E. coli* recovered from cooled carcasses were <3.1 and <2.2 log cfu 2500 cm^{-2}, respectively. The findings indicate that production processes for pig carcasses can be operated to give cooled carcasses with log mean numbers of total aerobes <2 cm^{-2}, and log total numbers of coliforms and *E. coli* each <1 2500 cm^{-2}.

Keywords: Pig carcasses; Processing hygiene; *Escherichia coli*; Contamination

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1. Introduction

At most plants where pigs are slaughtered, the carcasses are not skinned. Instead, before the carcasses are dressed they are subjected to the sequential operations of scalding, dehairing, singeing and polishing, which result in the skin begin visibly clean and largely free of hair. Despite the appearance, the polished carcasses may be relatively heavily contaminated with bacteria (Gill and Bryant, 1993). Additional bacteria may be deposited on the carcass during operations on the head or for removal of the intestines (Gill and Jones, 1997a), and the numbers of bacteria on the carcasses may reduce or increase during the carcass cooling process (Gill and Jones, 1997b). Thus, the hygienic effects of apparently similar processes at various plants may be very different. If such differences do exist they must be recognized if the actions to control the microbiological contamination of carcasses are to be appropriate at each plant (Gill, 1998). Therefore, the microbiological conditions of pig carcasses, after polishing, after dressing and after cooling at eight packing plants were assessed, for better understanding of the differences between the hygienic effects of current commercial processes for the production of pig carcasses.

2. Material and methods

2.1. The carcass production processes

Samples were obtained from carcasses at eight Canadian pork packing plants. The rates at which carcasses were processed ranged from about 200 to about 800 h^{-1} (Table 1). The carcasses were subjected to scalding, dehairing, singeing and polishing before dressing at all of the plants. At one plant only, the polished carcasses were pasteurized before dressing commenced. The dressed carcasses were blasted with air of about $-20°C$, for about 1 h during passage through a tunnel before entering a chiller at five of the plants, and the carcasses were sprayed with water during the first few hours of the cooling process at two of the plants.

2.2. Sampling of carcasses

Samples were collected from sites which were selected at random from a grid which specified 83 areas on one side of a carcass (Gill and Jones, 1997a). Samples were obtained from carcasses after they left the polisher, after the final wash in the dressing process, and after completion of the cooling process when carcasses were about to be or had been moved from the chiller, as was convenient at each plant. At each plant, on each of 5 days, five samples were collected from carcasses at each of the three stages of processing.

Table 1
The maximum rates of carcass processing, and the forms of the carcass cooling processes at the eight pork plants at which samples were collected from carcasses

Plant	Rate of processing (carcasses h^{-1})	Pasteurizing of polished carcasses	Blasting with freezing air	Spraying during cooling
A	460	−	+	−
B	250	−	−	−
C	600	−	−	+
D	330	−	−	−
E	180	−	+	−
F	480	−	+	−
G	480	−	+	−
H	800	+	+	+

Each sample was obtained by swabbing an undelimited area of approximately 100 cm^2 with a sterile gauze swab (5×5 cm, eight-ply, Curity gauze sponge; Kendall Canada, Peterborough, Ont., Canada), which had been moistened with 0.1% (w/v) peptone water (Difco Laboratories, Detroit, MI, USA). Carcasses to be swabbed, and the site to be swabbed on each were selected at random. A single sample from a randomly selected site was collected from the selected side of each selected carcass. Each swab was placed in a separate stomacher bag (Baxter Diagnostic, Edmonton, AB, Canada), which was then immersed in slush ice. Each sample was processed within 3 h of being collected.

2.3. Enumeration of bacteria

Each swab was stomached for 2 min with 10 or 25 ml of 0.1% (w/v) peptone water. Total aerobic counts were enumerated by a hydrophobic grid membrane filter (HGMF) procedure (plants A, B, C and H) or by a spread plate procedure, (plants D, E, F and G). For the HGMF procedure, 0.1 ml of the 10 ml volume of stomacher fluid was diluted into 10 ml

of 0.1% (w/v) peptone water, and 0.1 ml of that first dilution was diluted into a further 10 ml of peptone water. The whole of each dilution was filtered through a separate hydrophobic grid membrane filter (QA Life Sciences, San Diego, CA, USA). Each filter was placed on a plate of tryptone soy fast green agar (QA Life Sciences), which was incubated at 25°C for 3 days. Each filter was examined under $\times 5$ magnification using a model 101 Iso-Grid line counter (QA Life Sciences). Squares containing green or blue–green colonies were counted, and a most probable number for the colonies on each filter was obtained by application of the formula:

$$\text{MPN} = 1600\ [(\log_e(1600 \div 1600 - \text{square count})].$$

For the spread plate procedure, 1 ml of the 25 ml volume of stomacher fluid was used to prepare serial 10-fold dilutions, to 10^{-3}, then 0.1 ml of the undiluted fluid and of each dilution were spread on duplicate plates of plate count agar (Difco Laboratories, Detroit, MI, USA) which were incubated for 2 days at 25°C. Flora numbers were determined from plates bearing 20–200 colonies.

For the enumeration of coliforms and *Escherichia coli*, 0.1 ml of each stomacher fluid was diluted into 10 ml of peptone water. Then, the whole of the remaining, undiluted fluid and the dilution were each filtered through a separate hydrophobic grid membrane filter. Each filter was placed on a plate of lactose monensin gluconurate agar (QA Life Sciences) which was incubated at 35°C for 24 h. Squares containing blue colonies were counted, and a most probable number of coliforms were obtained as in the estimation of total aerobic counts by the HGMF procedure.

Each filter was then transferred to a plate of buffered 4-methylumbelliferyl-β-D-glucuronide agar (QA Life Sciences) which was incubated at 35°C for 3 h. The filters were examined under long-wavelength ultraviolet light. Squares containing large, blue–white, fluorescent colonies were counted, and a most probable number of *E. coli* was obtained as in the estimation of total aerobic counts by the HGMF procedure.

2.4. Analysis of data

Bacterial counts were arranged as sets of 25 values of one type obtained at each stage of processing at each plant. All counts were transformed to $\log_{10}$ values. When coliforms or *E. coli* were not detected in a sample, a log value of -0.5 100 cm^{-2} was assumed for the $\log_{10}$ count. For each set of log coliform or *E. coli* counts which contained ≤ 5 values of -0.5 100 cm^2, and for all sets of total aerobic counts, values for the mean $\log(\bar{x})$ and standard deviation (S.D.) were calculated on the assumption of a normal distribution of the log counts (Brown and Baird-Parker, 1982). A value for the $\log_{10}$ mean ($\log A$) for each of those sets of counts was also calculated, from the formula $\log A = \bar{x} + \log_n 10\ s^2/2$ (Kilsby and Pugh, 1981). A value for the $\log_{10}$ total number recovered (n) in each set was determined by summation of the counts in each set and transformation of the sum to the $\log_{10}$ value. Those calculations were performed using Microsoft Excel, Version 4, Statistical Functions (Microsoft, Redmond, WA, USA). Using SAS, version 6 (SAS Inst., Cary, NC, USA), a Wilk-Shapiro test for normal distribution was applied to each set of log values, and mean log values for sets of data of the same type obtained at each plant were separated by application of the Tukey option of the GLM procedure.

3. Results

A total aerobic count was obtained from every sample. Of the 24 sets of log total aerobic counts only three, each from a different plant, were not normally distributed (Table 2). For sets of total aerobic counts from each of the plants A, B, C, D, E and F, the log mean numbers on carcasses at the three stages of processing differed by <0.9 log units, and the log total numbers recovered at the three stages of processing differed by <0.7 log units. For each of plants A, B and E, the mean log numbers of total aerobic counts at the three stages of processing were not significantly different ($P>0.05$). For each of plants D and F the mean log numbers after polishing were significantly greater ($P<0.05$) than the mean log numbers after washing or cooling. For plant C, the mean log numbers after cooling were significantly less ($P<0.05$) than the mean log numbers after polishing or washing. For sets of total aerobic counts from plant A, B, C and D, all log mean numbers were within the range 3.5 ± 0.5, and

Table 2
Statistics for sets of 25 total aerobic counts (cfu cm^{-2}) obtained from pig carcasses at eight plants (1) after polishing, (2) after the final wash in the dressing process or (3) after cooling[a]

Plant	Stage of processing	Statistics			
		$\bar{x}$	S.D.	Log *A*	*n*
A	1	3.35*	0.46	3.60	4.96
	2	3.48*	0.51	3.78	5.12
	3	3.56*	0.42	3.76	5.19
B	1	2.95*	0.83	3.75	4.88
	2	2.94*	0.68	3.47	4.82
	3	2.56*	0.92	3.54	4.88
C	1	3.09*	0.63	3.54[c]	4.75
	2	2.84*	0.60	3.25	4.25
	3	2.69**	1.02	3.89	4.90
D	1	3.22*	0.73	3.83[c]	5.00
	2	2.64**	0.59	3.04	4.39
	3	2.69**	0.70	3.25	4.57
E	1	2.39*	0.35	2.53	3.89
	2	2.33*	0.41	2.54	3.99
	3	2.62*	0.70	3.18	4.57
F	1	2.67*	0.60	3.08	4.34
	2	1.93**	0.59	2.33	3.65
	3	1.67**	0.65	2.16	3.64
G	1	1.49*	0.58	1.88	3.26
	2	2.01*	0.68	2.54	3.85
	3	2.62**	1.08	3.54	5.33
H	1	2.22*	0.57	2.59	3.85
	2	1.06**	0.82	1.83	3.07
	3	2.04*	0.68	2.57***	3.71

[a] $\bar{x}$, mean log; S.D., standard deviation; log *A*, estimated log of the arithmetic mean; *n*, log total number recovered from 25 cm^2.
*,** within each group of three sets, mean logs with the same superscript are not significantly different ($P>0.05$); *** the set of log values is not normally distributed.

all log total numbers recovered were within the range 4.7 ± 0.5. For the sets of total aerobic counts from plants E, and F, the log mean numbers were in the ranges 2.9 ± 0.4 and 2.6 ± 0.5, respectively; and the log total numbers recovered were in the ranges 4.2 ± 0.4 and 4.0 ± 0.4, respectively.

For sets of total aerobic counts from plant G, both the log mean number and the log total number recovered after cooling were ≥1 log unit more than the corresponding numbers after polishing or after washing, and the mean log number was significantly greater ($P<0.05$) after cooling than after polishing or washing (Table 2). For sets of total aerobic counts from plant H, both the log mean number and the log total number recovered after washing were about 0.8 log unit less than the corresponding numbers after polishing, and the mean log number was significantly less ($P<0.05$) after washing than after polishing. However, the corresponding values for log mean numbers, log total numbers recovered and mean log numbers were similar after polishing or cooling.

A coliform count was obtained from ≥20 samples for only 12 of the 24 sets of samples (Table 3). Three of the 12 sets of counts for which a mean log, standard deviation and log mean could be calculated were not normally distributed. Two of those sets included assumed values for five samples which did not yield coliforms. At plants D and E, coliforms were recovered from most of the samples obtained at each stage of processing. At plants A, B, C, F and H, coliforms were recovered from majorities of the samples obtained after polishing or after washing, but from only minorities of the samples obtained after cooling. At plant G coliforms were recovered from a majority of samples only after washing.

At plants A, B and G, the log mean numbers and/or the log total numbers of coliforms recovered were each >1 log unit more after washing than after polishing (Table 3). At plants A and B the mean log numbers at those stages of processing were significantly different ($P>0.05$). After cooling, the log total numbers of coliforms recovered at plants A and G were >0.9 log unit less than the log total number recovered after washing. At plant B, the log total number of coliforms recovered after cooling was 0.5 log units more than the number recovered after washing, but that high value was the result of a single log count of 4.0, the log of the sum of the other coliforms counts being 1.86. At each of plants, C, D, E, F and H, the log mean numbers of coliforms were similar at each stage of processing. At plants C, D and E, mean log numbers at different stages of processing were not significantly different ($P>0.05$).

An *E. coli* count was obtained from ≥20 samples from only four of the 24 sets of samples (Table 4). One of the sets of counts obtained from those sets of samples was not normally distributed. That set of counts included assumed values for five samples which had not yielded *E. coli*. At most of the plants, the log total numbers of *E. coli* differed in the same

Table 3
Statistics for sets of 25 coliform counts (cfu 100 cm^{-2}) obtained from pig carcasses at eight plants (1) after polishing, (2) after the final wash in the dressing process or (3) after cooling[a]

Plant	Stage of processing	Statistics				
		$\bar{x}$	S.D.	No.	Log *A*	*n*
A	1	0.71*	0.76	5	1.38***	2.57
	2	2.09**	0.41	0	3.04	4.29
	3	–	–	14	–	2.50
B	1	0.52*	0.69	4	1.06	2.59
	2	1.14**	0.90	3	2.08	3.47
	3	–	–	14	–	4.01
C	1	1.37*	0.55	0	1.72	3.08
	2	1.12*	0.63	0	1.58	2.87
	3	–	–	15	–	2.50
D	1	1.25*	1.15	5	2.77***	3.36
	2	1.52*	0.85	0	2.35	3.59
	3	–	–	7	–	2.85
E	1	1.11*	0.94	3	2.13***	3.10
	2	1.01*	0.88	4	1.90	3.03
	3	1.32*	0.64	1	1.79	3.08
F	1	0.79	0.68	3	1.32	2.61
	2	–	–	10	–	2.48
	3	–	–	15	–	2.70
G	1	–	–	15	–	1.23
	2	–	–	6	–	2.99
	3	–	–	14	–	2.08
H	1	–	–	10	–	2.12
	2	–	–	12	–	2.14
	3	–	–	13	–	1.68

[a] $\bar{x}$, mean log; S.D., standard deviation; No., number of samples from which coliforms were not recovered; log *A*, estimated log of the arithmetic mean; *n*, log total number recovered from 2500 cm^2.

*,** within each group of three sets, mean logs with the same superscript are not significantly different ($P>0.05$); *** the set of log values is not normally distributed.

Table 4
Statistics for sets of 25 *Escherichia coli* counts (cfu 100 cm^{-2}) obtained from pig carcasses at eight plants (1) after polishing, (2) after the final wash in the dressing process or (3) after cooling[a]

Plant	Stage of processing	Statistics				
		$\bar{x}$	S.D.	No.	Log *A*	*n*
A	1	–	–	7	–	2.32
	2	1.62	0.88	1	2.52	3.75
	3	–	–	17	–	1.74
B	1	–	–	9	–	2.19
	2	0.63	0.89	5	1.53***	2.78
	3	–	–	17	–	3.68
C	1	1.08*	0.68	1	1.53	2.83
	2	0.81*	0.72	1	1.41	2.70
	3	–	–	16	–	2.12
D	1	–	–	11	–	2.45
	2	–	–	9	–	2.43
	3	–	–	18	–	1.38
E	1	–	–	11	–	2.45
	2	–	–	14	–	2.01
	3	–	–	15	–	1.99
F	1	–	–	19	–	1.28
	2	–	–	21	–	1.23
	3	–	–	22	–	1.04
G	1	–	–	23	–	0.48
	2	–	–	19	–	1.79
	3	–	–	20	–	1.20
H	1	–	–	12	–	2.06
	2	–	–	13	–	1.76
	3	–	–	18	–	1.43

[a] $\bar{x}$, mean log; S.D., standard deviation; No., number of samples from which *E. coli* were not recovered; log *A*, estimated log of the arithmetic mean; *n*, log total number recovered from 2500 cm^2.

*,** within each group of three sets, mean logs with the same superscript are not significantly different ($P>0.05$); *** the set of log values is not normally distributed.

manner as the log total numbers of coliform at the three stages of processing. That is, at plants A, B and G, the log total numbers of *E. coli* were >1 log unit more after washing than after polishing, and the log total numbers were smaller after cooling than after washing at plants A and G, but larger after cooling at plant B; while at plants C, E, F and H, the log total numbers recovered were similar at the three stages of processing. However, at plant D, the log total number of *E. coli* recovered after cooling was >1 log unit less than the corresponding log total numbers recovered after polishing and after washing, whereas the log total numbers of coliforms recovered were similar at all three stages of processing.

The fractions of coliforms which were *E. coli* differed between plants. At plants A, B, C and H, *E. coli* were generally >20%, and often about 50% or more of the coliforms recovered, whereas at plants D, E, F and G, *E. coli* were <20% and often <10% of the coliforms recovered (Table 5).

Table 5
Fractions of *Escherichia coli* in the coliforms recovered from pig carcasses at eight plants (1) after polishing, (2) after the final wash in the dressing process or (3) after cooling

Plant	Stage of processing	*E. coli* fraction (%)
A	1	64
	2	29
	3	17
B	1	40
	2	20
	3	47
C	1	56
	2	67
	3	42
D	1	12
	2	7
	3	3
E	1	18
	2	9
	3	8
F	1	5
	2	6
	3	2
G	1	18
	2	6
	3	13
H	1	86
	2	41
	3	50

4. Discussion

The variant procedures for enumerating bacteria at different laboratories were adopted to conform conveniently with the procedures that were routine at each laboratory. The differences in procedures would not significantly affect the numbers of bacteria recovered (Gill and Jones, 2000).

The approximation to a log normal distribution of the bacterial numbers in most sets of 25 counts obtained by the random sampling of carcasses was to be expected (Hildebrandt and Weiss, 1994b). The log normal distribution will not be approximated when an assumed value has to be assigned for each of five or more samples, of 25, which yield no bacteria (Gill et al., 1998b). Despite the deviation from log normality, it seems appropriate to calculate a value for the log mean when bacteria are not recovered from five of 25 samples, as the microbiological conditions of meat at different stages of processing are best compared by reference to that statistic (Kilsby, 1982). The microbiological condition of meat can also be assessed by reference to the log total numbers recovered from 25 samples, which tend to vary as the log mean numbers (Gill et al., 1998b), and must be assessed by reference to that statistic when the log mean numbers cannot be calculated. When the variances within different sets of log counts are similar, the statistical significance of the differences between log means can be assessed by reference to the significance of differences between mean logs. However, log values for bacterial numbers which do not differ by about one log or more must be regarded as similar for microbiological purposes, irrespective of the statistical significance of any difference (Jarvis, 1989). With those points in view the microbiological effects of carcass processing at each of the plants which was studied can be assessed.

At plant A, the numbers of total aerobes on the polished carcasses are unaffected by the dressing or cooling processes. That is, any bacteria added by dressing operations or the cooling process are no more and probably less than those that contaminate the polished carcasses, while any removed are few in comparison to the numbers on the polished carcasses. However, coliforms that include *E. coli* are deposited on the carcass during the dressing process. Before dressing, the coliforms on the carcasses are largely *E. coli*, which indicates they originate from faecal material deposited on the carcasses during the dehairing process (Gill and Jones, 1997a). After dressing the fraction of *E. coli* in the coliform population is lower, which suggests that many of the coliform organisms on the dressed carcass originate from the mouth and throats of carcasses, where *E. coli* are about 10% of the coliform population (Gill and Jones, 1998a). However, after cooling the numbers of coliforms and *E. coli* are reduced, which can be an effect of the drying of carcass surfaces when they are cooled without spraying, with *E. coli* being more susceptible to the lethal effects of drying than the coliform population as a whole (Gill and Jones, 1997b).

At plant B, the effects of processing on the microflora are similar to those at plant A. However, the single sample from cooled carcasses that yielded

a large number of coliforms that were largely *E. coli* suggests sporadic but possibly relatively frequent contamination with faecal material during either the dressing process or handling in the cooler.

At plant C, the microbiological conditions of the washed or cooled carcasses were little if any different from the condition of the polished carcasses, which indicates that the dressing and cooling processes are largely without effect on the carcass microflora. Containment but not reduction of bacterial numbers by a spray cooling process would be expected (Gill and Bryant, 1997). The microflora on carcasses at plants E and F also appear to be little affected by the dressing or cooling processes, but some reduction in *E. coli* numbers may result from the cooling process at plant D. The small fractions of *E. coli* in the coliform populations recovered from carcasses at those latter three plants suggest that those bacteria originate largely from the mouths of carcasses and/or equipment rather than from faecal matter (Gill and Jones, 1997a). At plant G, the relatively small numbers of bacteria on the polished carcasses are apparently augmented by bacteria deposited on the carcasses during the dressing process. The increased total counts on carcasses, with increased variance of the log values after cooling, but possibly decreased coliform and *E. coli* counts suggests that the cooling process is poorly controlled, with growth on some parts of some carcasses, but with drying of some other surfaces with consequent destruction of some coliforms.

At plant H, the numbers of bacteria on the polished carcasses are reduced by a pasteurizing treatment to log mean numbers of total aerobes about 1 cm^{-2}, and log total numbers of coliforms and *E. coli* about 0 2500 cm^{-2} (Gill et al., 1997). The bacteria found on the washed carcasses are then largely deposited during the dressing process. As at plant G, there may be relatively poor control of the cooling process with some growth of bacteria.

Actions for improving the microbiological conditions of carcasses of all species are focused on the carcass dressing processes (Soul, 1996; Cassin et al., 1998). Appropriate actions in that area could be effective for reducing the contamination of carcasses with coliforms and *E. coli* at plants A and B; and for reducing contamination with all bacteria at plants G and H, where the microbiological conditions of the polished or polished and pasteurized carcasses, respectively, are superior to the conditions of polished carcasses at other plants. However, at the other four plants, actions during dressing can do little if anything to improve the microbiological conditions of carcasses, which are essentially determined by the overall effect of the operations that precede dressing. For improvement of the microbiological conditions of carcasses at those plants, some decontaminating treatment, such as pasteurizing, at least after polishing but preferably after dressing as well, would be required (Gill et al., 1998a).

If the microbiological condition of carcasses is to improve, some microbiological target, or food safety objective is required. At present, the only recognized microbiological criteria for pig carcasses are those promulgated by the US Department of Agriculture, which involve *Salmonella* and *E. coli* (USDA, 1996). The USDA criterion for generic *E. coli* on cooled carcasses is in the form of a three-point attributes acceptance plan (Hildebrandt and Weiss, 1994a). Contamination with *E. coli* is defined as unacceptable if in any 13 samples obtained consecutively by the specified method, more than three yield *E. coli* at numbers >10 cfu cm^{-2}, or any yields *E. coli* at numbers $>10^4$ cfu cm^{-2}.

The specified method of sampling involves swabbing an area of 100 cm^2 at a site on each of the ham, belly and jowl on one side of each randomly selected carcass. The swabs from those assumedly most heavily contaminated areas of each carcass are combined, and *E. coli* are enumerated with a level of detection of 1 cfu 24 cm^{-2}. The methods of sampling and enumeration of *E. coli* used in this study obviously differ from those specified by the USDA. However, the findings of the study can be related to the USDA standard, as the total numbers of *E. coli* cfu recovered from sets of samples by the USDA-specified methods or the methods used in this study are similar (Gill and Jones, 1998b). That is because, although the latter methods involve sampling of lightly as well as heavily contaminated sites, the latter methods also involve enumerating all *E. coli* from each 100-cm^2 area rather than 8% of the *E. coli* from 300 cm^2.

By the USDA criterion, the number of *E. coli* recovered from a sample is acceptable if it does not exceed 240 cfu. In this study, only one sample from cooled carcasses, at plant B, yielded such numbers of *E. coli*. At each of the other plants, the total number

of *E. coli* recovered from 25 cooled carcasses did not amount to 240 cfu. The USDA *E. coli* criterion would then seem to have little relevance to the hygienic performances of most of the plants which were studied. Instead, it appears that a microbiological condition for cooled carcasses far superior to that indicated by the USDA criterion can be routinely attained, and is already attained at some plants. Provided that effective decontaminating treatments, such as pasteurizing treatments, are applied to polished and/or dressed carcasses, it would seem possible for pork packing plants to produce cooled carcasses with log mean numbers of total aerobic counts <2 cm^{-2}, and log total numbers of coliforms and *E. coli* recovered from 25 random samples each <1 2500 cm^{-2}. Such numbers can therefore be proposed as attainable targets against which to assess the performances of the HACCP systems that are currently being developed for pig carcass production processes.

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